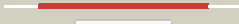
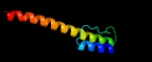

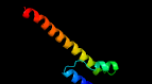

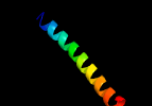



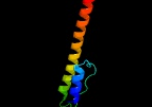

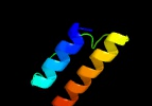
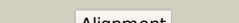
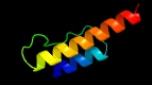





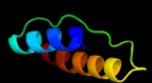

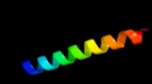

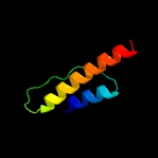
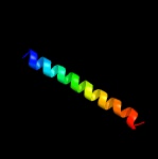
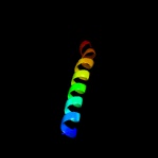
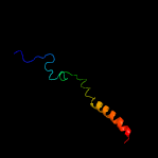
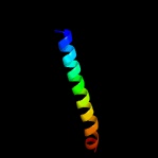
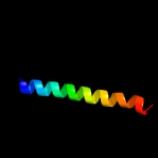
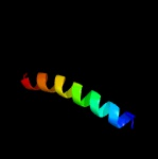
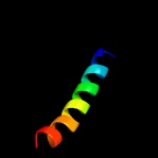



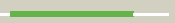



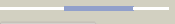


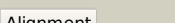
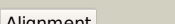




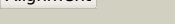
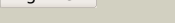
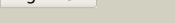
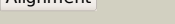
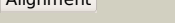
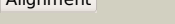
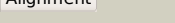
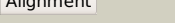
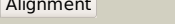
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2998A (-) _3357235_3357438
Date	Thu Aug 8 16:20:16 BST 2019
Unique Job ID	886b14d5fb0f766a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3zrwB_	 Alignment		99.7	22	PDB header: signaling protein Chain: B: PDB Molecule: af1503 protein, osmolarity sensor protein envz; PDBTitle: the structure of the dimeric hamp-dhp fusion a291v mutant
2	c4biuB_	 Alignment		99.2	25	PDB header: transferase Chain: B: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (orthorhombic form 1)
3	c4biyD_	 Alignment		98.8	36	PDB header: transferase Chain: D: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (monoclinic form 2)
4	c3zx6A_	 Alignment		98.8	17	PDB header: signaling Chain: A: PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
5	c3lnrA_	 Alignment		98.8	11	PDB header: signaling protein Chain: A: PDB Molecule: aerotaxis transducer aer2; PDBTitle: crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
6	d2asxa1	 Alignment		98.7	25	Fold: HAMP domain-like Superfamily: HAMP domain-like Family: HAMP domain
7	c4gn0D_	 Alignment		98.7	23	PDB header: signaling protein Chain: D: PDB Molecule: hamp domain of af1503; PDBTitle: de novo phasing of a hamp-complex using an improved arcimboldo method
8	c4ctiA_	 Alignment		98.7	23	PDB header: signaling protein Chain: A: PDB Molecule: osmolarity sensor protein envz, af1503; PDBTitle: escherichia coli envz histidine kinase catalytic part fused to2 archaeoglobus fulgidus af1503 hamp domain
9	c4mt8A_	 Alignment		98.4	22	PDB header: transferase Chain: A: PDB Molecule: ethylene response sensor 1; PDBTitle: structure of the ers1 dimerization and histidine phosphotransfer2 domain from arabidopsis thaliana
10	c5jefA_	 Alignment		98.4	20	PDB header: transferase Chain: A: PDB Molecule: nitrate/nitrite sensor protein narq; PDBTitle: fragment of nitrate/nitrite sensor histidine kinase narq (wt) in2 asymmetric holo state
11	c5ukvA_	 Alignment		98.2	48	PDB header: transferase Chain: A: PDB Molecule: atp-binding protein; PDBTitle: dhp domain of phor of m. tuberculosis - semet

12	d1joya_	Alignment		98.1	21	Fold: ROP-like Superfamily: Homodimeric domain of signal transducing histidine kinase Family: Homodimeric domain of signal transducing histidine kinase
13	c4i5sA_	Alignment		98.1	16	PDB header: transferase Chain: A: PDB Molecule: putative histidine kinase covs; vick-like protein; PDBTitle: structure and function of sensor histidine kinase
14	d2c2aa1_	Alignment		97.8	35	Fold: ROP-like Superfamily: Homodimeric domain of signal transducing histidine kinase Family: Homodimeric domain of signal transducing histidine kinase
15	c6nb0A_	Alignment		97.8	29	PDB header: transferase Chain: A: PDB Molecule: histidine kinase; PDBTitle: crystal structure of histidine kinase from burkholderia phymatum2 stm815
16	c2rm8A_	Alignment		97.7	21	PDB header: signaling protein Chain: A: PDB Molecule: sensory rhodopsin ii transducer; PDBTitle: the solution structure of phototactic transducer protein2 htrii linker region from natronomonas pharaonis
17	c4ew8A_	Alignment		97.6	36	PDB header: transferase Chain: A: PDB Molecule: sensor protein divl; PDBTitle: crystal structure of a c-terminal part of tyrosine kinase (divl) from2 caulobacter crescentus cb15 at 2.50 a resolution (psi community3 target, shapiro l.)
18	c2c2aA_	Alignment		97.3	37	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase; PDBTitle: structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
19	c5idjA_	Alignment		97.1	13	PDB header: transferase Chain: A: PDB Molecule: cell cycle histidine kinase ccka; PDBTitle: bifunctional histidine kinase ccka (domains dhp-ca) in complex with2 adp/mg2+
20	c4qpkA_	Alignment		96.6	23	PDB header: signaling protein Chain: A: PDB Molecule: phosphotransferase; PDBTitle: 1.7 angstrom structure of a bacterial phosphotransferase
21	c4fmtB_	Alignment	not modelled	95.9	9	PDB header: transferase Chain: B: PDB Molecule: chpt protein; PDBTitle: crystal structure of a chpt protein (cc_3470) from caulobacter2 crescentus cb15 at 2.30 a resolution
22	c3d36B_	Alignment	not modelled	95.2	33	PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: sporulation kinase b; PDBTitle: how to switch off a histidine kinase: crystal structure of2 geobacillus stearothermophilus kinb with the inhibitor sda
23	c4r39A_	Alignment	not modelled	94.7	15	PDB header: transferase Chain: A: PDB Molecule: blue-light-activated histidine kinase 2; PDBTitle: histidine kinase domain from erythrobacter litoralis el346 blue-light2 activated histidine kinase
24	c2q8fA_	Alignment	not modelled	91.8	5	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; PDBTitle: structure of pyruvate dehydrogenase kinase isoform 1
25	c3gieA_	Alignment	not modelled	90.9	20	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase desk; PDBTitle: crystal structure of desk_h188e in complex with amp-pcp
26	c3d2rB_	Alignment	not modelled	90.1	8	PDB header: transferase Chain: B: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; PDBTitle: crystal structure of pyruvate dehydrogenase kinase isoform 4 in2 complex with adp
27	d1ixma_	Alignment	not modelled	80.9	8	Fold: Sporulation response regulatory protein Spo0B Superfamily: Sporulation response regulatory protein Spo0B Family: Sporulation response regulatory protein Spo0B
28	c3crlB_	Alignment	not modelled	77.4	8	PDB header: transferase Chain: B: PDB Molecule: pyruvate dehydrogenase [lipoamide] kinase isozyme 2, PDBTitle: crystal structure of the pdhk2-l2 complex.

29	c1y8oA	 Alignment	not modelled	77.2	3	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; PDBTitle: crystal structure of the pdk3-l2 complex
30	c3tz5A	 Alignment	not modelled	57.7	17	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: [3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, PDBTitle: crystal structure of branched-chain alpha-ketoacid dehydrogenase2 kinase/phenylbutyrate complex with adp
31	c2bu8A	 Alignment	not modelled	42.4	7	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase kinase isoenzyme 2; PDBTitle: crystal structures of human pyruvate dehydrogenase kinase 2 containing2 physiological and synthetic ligands
32	c1gfvA	 Alignment	not modelled	41.6	17	PDB header: transferase Chain: A: PDB Molecule: [3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase; PDBTitle: branched-chain alpha-ketoacid dehydrogenase kinase (bck) complexed with2 atp-gamma-s
33	c2oo4B	 Alignment	not modelled	29.3	32	PDB header: cell cycle,signaling protein Chain: B: PDB Molecule: neurogenic locus notch homolog protein 2; PDBTitle: structure of Inr-hd (negative regulatory region) from human notch 2
34	c3etoB	 Alignment	not modelled	20.9	14	PDB header: signaling protein Chain: B: PDB Molecule: neurogenic locus notch homolog protein 1; PDBTitle: 2 angstrom xray structure of the notch1 negative regulatory region2 (nrr)
35	c3i08C	 Alignment	not modelled	18.3	13	PDB header: signaling protein Chain: C: PDB Molecule: neurogenic locus notch homolog protein 1; PDBTitle: crystal structure of the s1-cleaved notch1 negative2 regulatory region (nrr)
36	d1y2oa1	 Alignment	not modelled	17.9	17	Fold: BAR/IMD domain-like Superfamily: BAR/IMD domain-like Family: IMD domain
37	c4zlpB	 Alignment	not modelled	16.2	27	PDB header: transcription Chain: B: PDB Molecule: neurogenic locus notch homolog protein 3; PDBTitle: crystal structure of notch3 negative regulatory region
38	c4adsF	 Alignment	not modelled	14.9	13	PDB header: transferase/transferase Chain: F: PDB Molecule: pyridoxine biosynthetic enzyme pdx1 homologue, putative; PDBTitle: crystal structure of plasmodial plp synthase complex
39	c2zbtB	 Alignment	not modelled	13.3	7	PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
40	c6hyeF	 Alignment	not modelled	11.3	10	PDB header: plant protein Chain: F: PDB Molecule: pyridoxal 5'-phosphate synthase subunit pdx1.3; PDBTitle: pdx1.2/pdx1.3 complex (pdx1.3:k97a)
41	c6e95A	 Alignment	not modelled	10.9	10	PDB header: signaling protein Chain: A: PDB Molecule: staphylococcus aureus agrc histidine kinase module fused to PDBTitle: chimeric structure of saccharomyces cerevisiae gcn4 leucine zipper2 fused to staphylococcus aureus agrc cytoplasmic histidine kinase3 module (dataset isotropically truncated by hkl2000)
42	c4gczB	 Alignment	not modelled	10.4	26	PDB header: signaling protein, de novo protein Chain: B: PDB Molecule: blue-light photoreceptor, sensor protein fixl; PDBTitle: structure of a blue-light photoreceptor
43	c3zbhC	 Alignment	not modelled	9.6	15	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
44	c2nv2U	 Alignment	not modelled	8.6	8	PDB header: lyase/transferase Chain: U: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
45	c4b5pB	 Alignment	not modelled	7.9	23	PDB header: transferase Chain: B: PDB Molecule: alpha-tubulin n-acetyltransferase; PDBTitle: crystal structure of human alpha tubulin acetyltransferase2 catalytic domain q58a variant
46	c3rtyA	 Alignment	not modelled	7.8	7	PDB header: circadian clock protein Chain: A: PDB Molecule: period circadian protein; PDBTitle: structure of an enclosed dimer formed by the drosophila period protein
47	d1st6a4	 Alignment	not modelled	7.8	18	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
48	c3ok8A	 Alignment	not modelled	7.6	11	PDB header: protein binding Chain: A: PDB Molecule: brain-specific angiogenesis inhibitor 1-associated protein PDBTitle: i-bar of pinkbar
49	c3femB	 Alignment	not modelled	6.1	8	PDB header: biosynthetic protein, transferase Chain: B: PDB Molecule: pyridoxine biosynthesis protein snz1; PDBTitle: structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
50	c4iogD	 Alignment	not modelled	5.8	12	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
51	c2mn2A	 Alignment	not modelled	5.8	16	PDB header: antitoxin Chain: A: PDB Molecule: ymob; PDBTitle: 3d structure of ymob, a modulator of biofilm formation